

Appl. No. : 10/018,290
Filed : November 13, 2001

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NO:7, *Aquifex aeolicus* (A. aeoli) SEQ ID NO:8, *Escherichian coli* (E. coli) SEQ ID NO:9, *Salmonella typhimurium* (S. typhi) SEQ ID NO:10, *Chlamydia trachomatis* (C. trach) SEQ ID NO:11, *Streptococcus pyogenes* (S. pyoge) SEQ ID NO:12 and Sequence 1 from International Patent Publication No. WO97/01638) SEQ ID NO:13 are shown alligned with each other; gaps have been introduced to optimise alignment. Positions containing identical amino acid with respect to the OmpH sequence (SEQ ID NO:1) of *L. intracellularis* are shaded. Residues identical in all 10 sequences appear in boldface."

IN THE SEQUENCE LISTING

Please cancel from the application Original Sequence Listing pages 1-3 and substitute therefore the attached Replacement Sequence Listing pages 1-8.

REMARKS

This Response to the Notice Comply amends the Sequence listing to conform to requirements under the USPTO. The Sequence Listing and Specification were amended to add the sequences appearing in Figure 3. None of the above amendments incorporate new matter.

Enclosed herewith are: (1) a paper copy of the Replacement Sequence Listing, (2) and a computer readable version of the Replacement Sequence Listing. The Response to Notice to Comply directs entry of the paper copy of the Sequence Listing into the application. In view of the foregoing, the application is believed to fully comply with the Sequence Listing Disclosure requirements.

The changes made to the specification by the current amendment, including [deletions] and additions, are shown on an attached sheet entitled **VERSION WITH MARKINGS TO SHOW CHANGES MADE**, which follows the signature page of this Preliminary Amendment.

VERIFICATION UNDER 37 C.F.R. §1.821(f) & (g)

All of the sequences in the attached Sequence Listing were included in the application as filed. Pursuant to 37 C.F.R. §1.821(g), no new matter is being added herewith. As required under 37 C.F.R. §1.821(f), I hereby verify that the data on the enclosed disk and the paper copies of the Sequence Listing are identical.

Conclusion

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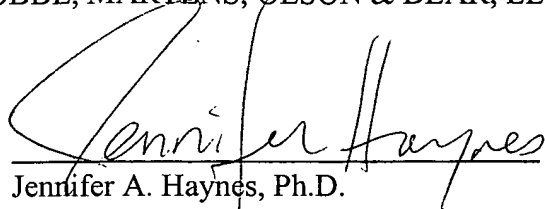
Should there be any questions concerning this application, the Examiner is respectfully invited to contact the undersigned at the telephone number appearing below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: April 11, 2002

By:


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**VERSION WITH MARKINGS TO SHOW CHANGES MADE
IN THE SPECIFICATION**

On page 8, third complete paragraph, lines 15-24, please replace the figure legend for Figure 3 with the following:

--**Figure 3** is a schematic representation of an amino acid sequence alignment of various bacterial outer membrane H proteins. Amino acid sequences of OmpH from *Lawsonia intracellularis* (L.int) SEQ ID NO:1, *Yersinia pseudotuberculosis* (Y. pseud) SEQ ID NO:5, *Yersinia enterocolitica* (Y. enter) SEQ ID NO:6, *Haemophilus influenzae* (H. influ) SEQ ID NO:7, *Aquifex aeolicus* (A. aeoli) SEQ ID NO:8, *Escherichian coli* (E. coli) SEQ ID NO:9, *Salmonella typhimurium* (S. typhi) SEQ ID NO:10, *Chlamydia trachomatis* (C. trach) SEQ ID NO:11, *Streptococcus pyogenes* (S. pyoge) SEQ ID NO:12 and Sequence 1 from International Patent Publication No. WO97/01638) SEQ ID NO:13 are shown aligned with each other; gaps have been introduced to optimise alignment. Positions containing identical amino acid with respect to the OmpH sequence (SEQ ID NO:1) of L. intracellularis are shaded. Residues identical in all 10 sequences appear in boldface."

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